

FIG. 1A

1	CGCCAAACCTCTATGGATATATAAGGGAAGCTTGAGGAGGAATTTCACAGTTACAGTGC	60
61	AGAAGCAGAGGCAAAAGAAATTAAACAGCTCTTCAGTCAAGCAAAATCCTCTACTCACCATG	120
	<u>M</u>	1
121	CTTCCTCCTGCCATTTCATTCTATCTCCTTCCCTTGCAATGCATCCTAATGAAAAGCTGT	180
2	<u>L P P A I H F Y L L P L A C I L M K S C</u>	21
181	TTGGCTTTTAAAAATGATGCCACAGAAAATCCTTTATTCACATGTGGTTAAACCTGTTCCA	240
22	<u>L A F K N D A T E I L Y S H V V K P V P</u>	41
241	GCACACCCAGCAGCAACAGCACGTTGAATCAAGCCAGAAATGGAGGCAGGCATTTCAGT	300
42	A H P S S N S T L N Q A R N G G R H F S	61
301	AACACTGGACTGGATCGGAACACTCGGGTTCAAGTGGGTTGCCGGGAACTGCGTTCCACC	360
62	N T G L D R N T R V Q V G C R E L R S T	81
361	AAATACATCTCTGATGGCCAGTGCCAGCATCAGCCCTCTGAAGGAGCTGCTGTGCT	420
82	K Y I S D G Q C T S I S P L K E L V C A	101

FIG. 1B

421 GCGAGTGTCTGCCCCCTGCCAGTGTCTCCCTAACTGGATTGGAGGAGGCTATGGAACAAAG 480
 102 G E C L P L P V L P N W I G G G Y G T K 121

 481 TACTGGAGCAGGAGGAGCTCCCAGGAGTGGCGGTGTGTCAATGACAAAACCCGTACCCAG 540
 122 Y W S R R S S Q E W R C V N D K T R T Q 141

 541 AGAATCCAGCTGCAGTGCCCAAGATGGCAGCACACGCACCTACAAAATCACAGTAGTCACT 600
 142 R I Q L Q C Q D G S T R T Y K I T V T 161

 601 GCCTGCAAGTGCAAGAGGTACACCCGGCAGCACAAACGAGTCCAGTCACAACTTTGAGAGC 660
 162 A C K C K R Y T R Q H N E S S H N F E S 181

 661 ATGTCACCTGCCAAGCCAGTCCAGCATCACAGAGAGCGGAAAGAGCCAGCAAAATCCAGC 720
 182 M S P A K P V Q H H R E R K R A S K S S 201

 721 AAGCACAGCATGAGTTAGAACTCAGACTCCCCATAACTAGACTTACTAGTAACCATCTGCT 780
 202 K H S M S * 206

 781 TTACAGATTGTGCTTGGAAGACTCAAGCCTGCCACTGCTGTGTTTCTCACTTGAAAGT 840
 841 ATATGCTTTCGTCTTGATCAAAACCCAGCAAGCTGTCTTAAAGTATCAGGACCTTCTTTGG 900

FIG. 2A

cyr6_mouse	1.....	M SSSFTFRTLAV	AVTLLHLTRL	AL.STCP.	AACHCP..
HCGF	M SSRIVRELAL	VVTLLHLTRV	GL.STCP.	ADCHCP..
ce10_chick	M GSAGARP.AL	AAALLCLARL	ALGSPCP.	AVCQCP..
ctgf_human	MTA ASMGPRVRAF	VVLLALCSRP	AVGQNCS.	GPCRCPD.
fisp-12	MLA SVAGPISLAL	.VLLALCTRP	ATGDQCS.	AQCQCAA.
nov_chick	METGGG....	...QGLPVLL	LLLLLLLRPCE	VSGREAA.	CPRPCGGR
HNGF	MQSVQSTSF	C LRKQCLCLTF	LLLHLLGQVA	ATQR.....	CPPQCPCR
VIGFMKSVL	LLTTLLVPAH	LVAAWSNNYA	VDCPQHCDSS	
ibp3_humanMQR	ARPTLWAAAL	TLLVLLRGPP	VARAGASSGG	LGPVVRCEPC	
SCGF

111	cyrr6_mouse	GLECNFGASS	TALKGICRAQ	SEGRPCEYNS	RIYQNGESFQ	PNCKHQCTCI	160
	HCGF	GLECNFGASS	TALKGICRAQ	SEGRPCEYNS	RIYQNGESFQ	PNCKHQCTCI	
	ce10_chick	GLECNFGASP	AATNGICRAQ	SEGRPCEYNS	KIYQNGESFQ	PNCKHQCTCI	
	ctgf_human	GLFCDFGSPA	NRKIGVCTAK	.DGAPCIFGG	TVYRSGESFQ	SSCKYQCTCL	
	fisp-12	GLFCDFGSPA	NRKIGVCTAK	.DGAPCVFVG	SVYRSGESFQ	SSCKYQCTCL	
	nov_chick	GLYCDRGPED	GGGAGICMVL	.EGDNCVFDG	MIYRNGETFQ	PSCKYQCTCR	
	HNGF	GLYCDRSADP	SNQTGICTAV	.EGDNCVFDG	VIYRSGEKFQ	PSCKFQCTCR	
	VIGF	GE...DPFG	EEFGICKDCP	YGT...FG	MDCRETCNCQ	SGICDRGTGK	
	libp3_human	DEARPLQALL	DGRGLCVNAS	AVSRLRAYLL	PAPPAPGNAS	ESEEDRSAGS	
	SCGF	

FIG. 2B

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51..... 110
..LEAPKCAP GVGLVR... DGCGCKVC AKQLNED... C SKTQPCDHTK
..LEAPKCAP GVGLVR... DGCGCKVC AKQLNED... C RKTQPCDHTK
..AAPQCAP GVGLVP... DGCGCKVC AKQLNED... C SRTQPCDHTK
..EPAPRCPA GVSLVL... DGCGCCRV C AKQLGEL... C TERDPCDPHK
..EAPHCPA GVSLVL... DGCGCCRV C AKQLGEL... C TERDPCDPHK
CPAEPPTCAP GVPAVL... DGCGCCLV C ARQGES... C SPLPCDESG
CPATPPTCAP GVR AVL... DGSCCCLV C ARQGES... C SDLEPCDESS
ECKSSPRCKR TVL..... DDCGCCRV C AAGRGETCYR TVSGMDGMKC GPGLRCQPSN
DARALAQCAP PPAVCAELVR EPGCGCLTC ALSEGQPC... GIYTERC GSGLRCQPSP
.....

161..... 220
D.GAVGCIPL CPQELSLPNL GCPNPRLVKV SGQCCCEWVC DEDSIKDSLD DQDDL...L
GWRRGACIPL CPQELSLPNL GCPNPRLVKV TGQCCCEWVC DEDSIKDPME DQDGLLGKGL
D.GAVGCIPL CPQELSLPNL GCPSPRLVKV PGQCCCEWVC DES..KDALE ELEGGFFSKEF
D.GAVGCMPL CSMDVRLPSP DCPFPRRVKL PGKCCCEWVC DEP..... KDQTVVGP
D.GAVGCVPL CSMDVRLPSP DCPFPRRVKL PGKCCKEWVC DEP..... KDR TAVGP
D.GQIGCLPR CNLGLLLPGP DCPFPRKIEV PGECCEKWVC DPR..... DEVLLGGF
D.GQIGCVPR CQLDVLLPEP NCPAPRKVEV PGECCEKWIC GPD..... FEEDSLGGL
CL..... KFPFFQYS VTKSSNRFVS LTHEDMASGD GNIVREEVVK
VESPSVSSSTH RVSDPKFHPL HSKIIIIKKG HAKDSQRYK.. VDYESQSTD TQNFSSSKR
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FIG 2.C

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221..... 270
cyr6_mouse GLDASEVELT RNNELIAIGK GSSLKRLLPVF GTEP.:RVLF NPLHAHQKC
      HCGF GFDASEVELT RNNELIAVGK GSSLKRLLPVF GMEP..RILY NPL...QGQKC
ce10_chick GLDASEGELT RNNELIAIVK G.GLKMLPVF GSEPQSRAFE NP.....KC
ctgf_human ALAAAYRLEDT .....F GPDPTMI... ..RANC
fisp-12 ALAAAYRLEDT .....F GPDPTMM... ..RANC
nov_chick AMAAYRQEAT .....L GIDVSDS... ..SANC
      HNGF TLAAAYRPEAT .....L GVEVSDS... ..SVNC
      VIGF ENAAGSPVMR KWLNPR..... ..
ibp3_human ETEYGPCCRRE MEDTLNHLKF LNVLSPRGVH IPNCDKKGFY KKKQCRPSKG
      SCGF ...MLPPATH FYLLPLACIL MKSCLAFKND ATEILYSHVV KPVPAHPSSN

331..... 380
cyr6_mouse TKKSPEPVRF TYAGCSSVKK YRPKYCGSCV DGRCCCTPLQT RTVKMRFRCE
      HCGF TKKSPEPVRF TYAGCLSVKK YRPKYCGSCV DGRCCCTPQLT RTVKMRFPCE
ce10_chick TKKSPSPVRF TYAGCSSVKK YRPKYCGSCV DGRCCCTPQQT RTVKIRFRCD
ctgf_human TPKISKPIKF ELSGCTSMKT YRAKFCGVCT DGRCCCTPHRT TTLPVEFKCP
fisp-12 TPKIAKPVKF ELSGCTSVKT YRAKFCGVCT DGRCCCTPHRT TTLPVEFKCP
nov_chick TKKSMKAVRF EYKNCTSVQT YKPRYCGLCN DGRCCCTPHNT KTIQVEFRCP
      HNGF TKKSLKAIHL QFKNCTSLHT YKPRFCGVCS DGRCCCTPHNT KTIQAEFQCS
      VIGF ..... ..
ibp3_human ..... ..
      SCGF ...PLPVLP NWIGGGYGTK YWSR...RSS QEWRCVNDKT RTQRIQLQCQ

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FIG 2D

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271..... 330
IVQTTWSQC SKSCGTGIST RVTNDNPECR LVKETRICEV RPCGQPVY.S SLKKGKKCSK
IVQTTWSQC SKTCGTGIST RVTNDNPECR LVKETRICEV RPCGQPVY.S SLKKGKKCSK
IVQTTWSQC SKTCGTGIST RVTNDNPDCK LIKETRICEV RPCGQPSY.A SLKKGKKCTK
LVQTTWSAC SKTCGMGIST RVTNDNASCR LEKQSRLLCMV RPCEADLEE. NIKKGKKCIR
LVQTTWSAC SKTCGMGIST RVTNDNTFCR LEKQSRLLCMV RPCEADLEE. NIKKGKKCIR
IEQTTWSAC SKSCGMGFST RVTNRNQCE MVKQTRLMM RPCEN..EEP SDKKGKKCIQ
IEQTTWTAC SKSCGMGFST RVTNRNRQCE MLKQTRLMMV RPCEQEPEQP TDKKGKKCLR
.....
RKRGFWCVD KYGQPLPGYT TKGKEDVHCY SMQSK.....
STLNQARNGG RHFSNTGL.D RNTRVQVGCR ELRSTKYISD GQCTISISPLK ELVCAGECL.

381..... 440
DGEFMSKNVM MIQSKKCNYN CPHPNEASFR LYSLFNDIHK FRD.....
DGETFSKNVM MIQSSKCNYN CPHANEAFFP FYRLF.....
DGETFTKSVM MIQSCRCNYN CPHANEA.YP FYRLVNDIHK FRD.....
DGEVMKKNNM FIKTCACHYN CPGDND.IFE SLYYRKMYGD MA.....
DGEIMKKNNM FIKTCACHYN CPGDND.IFE SLYYRKMYGD MA.....
QGKFLKKPMM LINTCVCHGN CPQSNNAFFQ PLDPMSEAK I.....
PGQIVKKPVM VIGTCTHTN CPKNNEAFLQ ELELKTTRGK M.....
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DGSTRYKIT VVTACKCKRY TRQHNESHN FESMSPAKPV QHHRERKRAS KSSKHSMS

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